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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/566,201	01/27/2006	Artur Pfitzner	MBP-033XX	8282

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EXAMINER	
BAGGOT, BRENDAN O	
ART UNIT	**PAPER NUMBER**
1638	

MAIL DATE	DELIVERY MODE
06/21/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/566,201	PFITZNER ET AL.	
	Examiner	Art Unit	
	Brendan O. Baggot	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 March 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-16 and 18-33* is/are pending in the application.

4a) Of the above claim(s) *15,16,18,19 and 29-33* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-14 and 20-28* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *27 January 2006* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *1/27/06; 3/26/06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Restriction / Election

1. Applicant's election with traverse of Applicant elects Group I, claims 1-14, 20-28, and SEQ ID NO: 1 only, in the reply filed on 3/16/07 is acknowledged. The traversal is on the ground(s) that "...not seen as ...undue burden ....". This is not found persuasive because while a search of the prior art for one group may overlap with that of another group, they are not co-extensive of each other and thus would represent undue burden on Office resources.

2. Claims 15-16, 18-19, 29-33 and sequences other than SEQ ID NO: 1 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 3/16/07.

3. Claims 1-14, 20-28 are examined in the instant application.

4. The requirement is deemed proper and is therefore made FINAL.

Sequence Listing

5. Applicant's computer readable format sequence listing has been entered.

Drawings

6. The drawings are acceptable for examination.

Claim Objections

7. Claim 1 is objected to because of the following informalities: the claim recites non-elected SEQ ID NOs. Appropriate correction is required.

8. Claims 9, 21 are objected to because of the following informalities: the claim recites the ". . . host organism ... is ... a plant cell." Plant cells are not organisms. Appropriate correction is required.

9. Claim 1 is objected to because of the following informalities: the claim recites an improper Markush group drawn to 2 members of a genus and a separate genus. Appropriate correction is required.

Claim Rejections - 35 U.S.C. §112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

10. Claims 1-14 and 20-28 rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention.

11. In Claims 1-14 and 20-28, it is unclear what is being retained in the derived product.

Claim Rejections - 35 USC § 112, 1st, paragraph, written description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the

art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

A description of a genus of cDNAs may be achieved by means of a recitation of a *representative number* of cDNAs, defined by nucleotide sequence, falling within the scope of the genus *or* of a recitation of *structural features* common to the members of the genus, which features constitute a substantial portion of the genus. *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398 (Fed. Cir. 1997). (emphasis added).

See also *Fiddes v. Baird*, 30 USPQ2d 1481 (Bd. Pat. App. & Int. 1993); *In re Curtis*, 69 USPQ2d 1274, 1282 (Fed. Cir. 2004); *Fiers v. Revel*, 25 USPQ2d 1601 (Fed. Cir. 1993); *Amgen Inc. v. Chugai Pharmaceutical.*, 18 USPQ2d 1016 (Fed. Cir. 1991).

12. Claims 1-14 and 20-28 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn to an inducible promoter, SEQ ID NO: 1 (NIMIN-1 promoter), biologically active derivatives of SEQ ID NO: 1 of any length and sequence from any source, "chemicals" and "organic compounds" capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant NIMIN-1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter which has any biological activity of any kind, including irreversible self-excision from the genome.

In contrast, Applicant has only described SEQ ID NO: 1(sequence listing), GUS expression data with NIMIN-1 (SEQ ID NO: 1)-GUS fusions (Examples 2-3), and transgenic tobacco plants containing SEQ ID NO: 1-GUS constructs(Examples 2-3).

Applicant does not describe biologically active derivatives of SEQ ID NO: 1 of any length and sequence from any source, any "chemicals" (e.g., mercury or water) or any "organic compounds" (e.g., cyanide or glyphosate) capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant SEQ ID NO: 1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter with any or no promoter activity.

Applicant has not described the structure or any other relevant characteristics for all nucleic acid sequences encoding biologically active derivatives of NIMIN-1 promoters, or a representative number of same and a literature review does not indicate that they are well known to one of skilled in the art. Applicant has only described nucleic acid sequences encoding SEQ ID NO: 1 from *Arabidopsis.*

Applicant fails to describe a representative number of biologically active derivatives of SEQ ID NO: 1, or chemicals or organic compounds capable of inducing said biologically active derivatives. Applicant only describes SEQ ID NO: 1. Furthermore, Applicant fails to describe structural features common to members of the claimed genus of biologically active derivatives of SEQ ID NO: 1. Hence, Applicant fails to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for NIMIN-1 promoter

activity, it remains unclear what features identify NIMIN-1 promoters. Since the genus of NIMIN-1 promoters or the genus of biologically active fragments thereof has not been described by either specific structural features or a representative number of species, the specification fails to provide an adequate written description to support the breath of the claims.

The Federal Circuit has clarified the application of the written description requirement. The court stated that a written description of an invention "requires a precise definition, such as by structure, formula, [or] chemical name, of the claimed subject matter sufficient to distinguish it from other materials." *University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1568; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997); *See also Fiddes v. Bair*d, 30 USPQ2d 1481 (Bd. Pat. App. & Int. 1993). The court also concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." *Eli Lilly*. Further, the court held that to adequately describe a claimed genus, Patent Owner must describe a representative number of the species of the claimed genus, and that one of skill in the art should be able to "visualize or recognize the identity of the members of the genus." *Id.*

Finally, the court held:

> A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus. *Id.*

See also MPEP Section 2163, page 174 of Chapter 2100 of the August 2005 version, column 1, bottom paragraph, where it is taught that

> [T]he claimed invention as a whole may not be adequately described where an invention is described solely in terms of a method of its making coupled with its function and there is no described or art-recognized correlation or relationship between the structure of the invention and its function. A biomolecule sequence described only by a functional characteristic, without any known or disclosed correlation between that function and the structure of the sequence, normally is not a sufficient identifying characteristic for written description purposes, even when accompanied by a method of obtaining the claimed sequence.

See also Amgen Inc. v. Chugai Pharmaceutical Co. Ltd., 18 USPQ 2d 1016 at 1021, (Fed. Cir. 1991) where it is taught that a gene is not reduced to practice until the inventor can define it by "its physical or chemical properties" (e.g. a DNA sequence).

Given the claim breadth and lack of guidance as discussed above, the specification fails to provide an adequate written description of the genus of sequences as broadly claimed. Given the lack of written description of the claimed genus of sequences, any method of using them, such as transforming plant cells and plants therewith, and the resultant products including the claimed transformed plant cells and plants containing the genus of sequences, would also be inadequately described. Accordingly, one skilled in the art would not have recognized Applicant to have been in possession of the claimed invention at the time of filing. *See* The Written Description Requirement guidelines published in Federal Register/ Vol. 66, No. 4/ Friday January 5, 2001/ Notices: pp. 1099-1111.

Claim Rejections - 35 U.S.C. §112, first paragraph, enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

13. Claims 1-14 and 20-28 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for SEQ ID NO: 1, does not reasonably provide enablement for biologically active derivatives of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The *Wands* court set forth the enablement balancing test:

> Factors to be considered in determining whether a disclosure meets the enablement requirement of 35 USC 112, first paragraph, have been described by the court in *In re Wands*, 858 F.2d 731, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). *Wands* states at page 1404, "Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in Ex parte Forman. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the 'claims."

M.P.E.P. § 2164.01(a); *See also Ex Parte Forman* 230 USPQ 546, 547 (BdPatAppInt 1986); *See also Enzo Biochem, Inc., v. Calgene, Inc.*, 188 F.3d 1362, 52 USPQ2d 1129 (Fed. Cir. 1999).

The claims are broadly drawn to an inducible promoter, SEQ ID NO: 1 (NIMIN-1 promoter), biologically active derivatives of SEQ ID NO: 1 of any length and sequence

from any source, "chemicals" and "organic compounds" capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant NIMIN-1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter which has any biological activity of any kind, including irreversible self-excision from the genome.

In contrast, Applicant has only teaches SEQ ID NO: 1(sequence listing), GUS expression data with NIMIN-19 (SEQ ID NO: 1)-GUS fusions (Examples 2-3), and transgenic plants containing SEQ ID NO: 1-GUS constructs(Examples 2-3).

Applicant do not teach biologically active derivatives of SEQ ID NO: 1 of any length and sequence from any source, "chemicals" (e.g., mercury or water) or "organic compounds" (e.g., cyanide or glyphosate) capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant SEQ ID NO: 1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter which somehow "modulates" expression or activity of a gene of interest.

The Breadth Of The Claims

See above.

The Unpredictability of the Art and the State of the Prior Art

The state-of-the-art is such that one of skill in the art cannot predict which "biologically active derivatives of SEQ ID NO: 1" will work *a priori*. Reviews by Kim,

Hannenhalli, Maiti, and Doelling detail a variety of problems seen in promoter identification and modification.

The state of the prior art, as exemplified by Kim et al (Plant Molecular Biology, vol. 24, pp. 105-117, 1994)) teaches the extreme sensitivity of promoter regions to single base pair changes, the absolute requirement for as few as 3 to 6 nucleotides for promoter function, and the failure of a promoter to function either constitutively or specifically when lacking oligonucleotide regions approximately 100 bp upstream of the transcription start site (page 106, paragraph bridging the columns; paragraph bridging pages 107 and 108; page 110, paragraph bridging the columns). In addition, the claimed nucleic acid sequence that is a biologically active derivatives of SEQ ID NO: 1 would comprise non- functional transcriptional and translational elements, i.e. modifications of CAAT, TATA and the ATG codon, required for proper initiation of these cellular activities, known in the prior art; as well as highly conserved promoter regions rendered inactive by modifications. In addition, Applicant has not shown that any biologically active derivative of SEQ ID NO: 1 can also have the desired promoter activity.

A recent review by Hannenhalli (2001) Bioinformatics 17: S90-S96) teaches that prediction of eukaryotic promoters has been one of the most elusive problems despite considerable effort devoted to the study. (*See* the abstract at least). In the instant case of a promoter, Hannenhalli's review teaches a 50% failure in the sensitivity of promoter detection (p. S90, last full sentence).

Twenty base-pair long regions of a DNA fragment that has promoter activity cannot predictably be assumed to also have promoter activity. Deletion analysis of various promoters have shown that even DNA segments from the portion of a promoter region containing sequence elements thought to be most important (*e.g.*, the TATA-box) need to be longer than 20 basepairs. Maiti et al, in studies on a figwort mosaic virus promoter, found that the smallest portion upstream of the transcriptional start site that would support transcription was 198 basepairs long; segments of 73 and 37 basepairs did not work (1997, Transgen. Res., 6:143-156, see Fig. 4). Doelling et al found that the minimal rRNA promoter of *Arabidopsis thaliana* is at least 33 nucleotides long (1995, Plant J. 8:683-692, see Fig. 1).

Guidance in the Specification

See above. The specification, while suggesting the use of the SEQ ID NO: 1, did not provide significant guidance on how to overcome art recognized problems in achieving expression of promoter smaller "biologically active derivatives of SEQ ID NO: 1" of DNA, including single base pair polynucleotide promoters while still retaining activity.

In addition, since the working examples disclosed in the specification are limited to unmodified SEQ ID NO: 1, the chemically inducible activity of sequences cannot be extrapolated to any derivatives thereof, absent specific guidance. While Applicant is not required to exemplify each and every claimed embodiment, specific guidance as to

which region of the disclosed sequences can be modified, truncated so that the s chemically inducible activity promoter activity is retained is required.

The specification has no working examples of sequences other than SEQ ID NO: 1 and no working examples of any "biologically active derivatives of SEQ ID NO: 1".

Without sufficient guidance, identification of NIMIN-1 promoters is unpredictable and without guidance on how to overcome the problems seen in determining *a priori* which sequences will have NIMIN-1 promoter activity transgenic plants, it is unpredictable and the experimentation left to those skilled in the art is unnecessarily and improperly extensive and undue.

Therefore, given the breadth of the claims; the lack of guidance and working examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue trial and error experimentation would be required to practice the claimed invention, and therefore the invention is not enabled throughout the broad scope of the claims.

Claim Rejections - 35 U.S.C. §102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

35 U.S.C. §102.

14. Claims 1-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Sato,S., (2000) Structural analysis of *Arabidopsis thaliana* chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones. J. DNA Res. 7 (2), 131-135. (*See* Appendix A). Sato discloses a recombinant nucleic acid containing at least a first nucleotide sequence operably linked to at least a second nucleotide sequence containing a transgene to be expressed, wherein the first nucleotide sequence contains a regulatory sequence selected from the group consisting of SEQ-ID-No. I, and a biologically active derivative thereof, wherein the regulatory sequence is a promoter sequence selectively inducible by chemicals, wherein the chemicals are selected from the group consisting of organic compounds, wherein the organic compounds are selected from the group consisting of phenolic compounds, thiamine, benzoic acid, isonicotinic acid (INA), and derivatives thereof, wherein the phenolic compound is salicylic acid or a structural or functional derivative thereof, wherein the expression/transcription of said nucleotide sequence results in a detectable signal, a vector containing the recombinant nucleic acid according, and a bacterial host cell. (*Id.* @ p. 131, left column, 1st paragraph). Because Sato discloses cloning bugs with cloning vectors, Sato discloses the limitations of the claimed invention. Thus, the reference discloses all the limitations of the Claimed invention.

15. Claims 1-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Federspiel et al, (Database EMBL, 7 February 2000, Federspiel: Arabidopsis thaliana chromosome I BAG T14P4 genomic sequence, complete sequence. Database accession no. AC022521, *See* Appendix B) discloses a recombinant nucleic acid

containing at least a first nucleotide sequence operably linked to at least a second nucleotide sequence containing a transgene to be expressed, wherein the first nucleotide sequence contains a regulatory sequence selected from the group consisting of SEQ-ID-No. I, and a biologically active derivative thereof, wherein the regulatory sequence is a promoter sequence selectively inducible by chemicals, wherein the chemicals are selected from the group consisting of organic compounds, wherein the organic compounds are selected from the group consisting of phenolic compounds, thiamine, benzoic acid, isonicotinic acid (INA), and derivatives thereof, wherein the phenolic compound is salicylic acid or a structural or functional derivative thereof. Thus, the reference discloses all the limitations of the Claimed invention.

16. Claims 1-14 and 20-28 are rejected under 35 U.S.C. 102(b) as being anticipated by Lebel et al discloses chemically inducible genes inducible by salicylic acid and uses thereof (Lebel, et al WO 98 03536 A1/1998, SEQ ID NO: 1, page 5, paragraph 2, lines 2-6).

Lebel discloses a recombinant nucleic acid containing at least a first nucleotide sequence operably linked (See claim 5) to at least a second nucleotide sequence containing a transgene to be expressed, wherein the first nucleotide sequence contains a regulatory sequence selected from the group consisting of a biologically active derivative SEQ-ID-No. I (See sequence listing), wherein the regulatory sequence is a promoter sequence selectively inducible by chemicals (See claim 1(a-c)), wherein the chemicals are selected from the group consisting of organic compounds (See page 2, line 9, 21-25), wherein the organic compounds are selected from the group consisting of

phenolic compounds, thiamine, benzoic acid, isonicotinic acid (INA), and derivatives thereof (See abstract, page 2, line 9, 21-25, page 10, line 6-26), wherein the phenolic compound is salicylic acid (See abstract) or a structural or functional derivative thereof (See abstract, page 2, lines 9, 21-25; page 10, lines 6-26), wherein the expression/transcription of said nucleotide sequence results in a detectable signal (claim 8; page 9, lines 18-26), a vector (claim 10) containing the recombinant nucleic acid, a host organism (claim 10), a bacterial or plant cell (claim 10), a transgenic plant wherein the recombinant nucleic acid is stably integrated into the genetic material (claim 10), wherein the transgene contained in the second nucleotide sequence is transiently expressed (*See* page 13, lines 9-18; note that the expression is measured in minutes), and wherein the expression of the transgene contained in the second nucleotide sequence is selectively induced upon treatment with chemicals (*See* page 14, lines 20-25).

Biologically active fragment is interpreted to encompass a single nucleotide base pair.

Thus the reference anticipates the claimed invention.

17. No Claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Brendan O. Baggot whose telephone number is 571/272-5265. The examiner can normally be reached on Monday - Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on 571/272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Brendan O. Baggot
Patent Examiner
Art Unit 1638

David H. Kruse, PhD
Primary Examiner
Art Unit 1638

DAVID H. KRUSE, PH.D.
PRIMARY EXAMINER

bob

APPENDIX A

SCORE Search Results Details for Application 10566201 and Search Result us-10-566-201-2.rge.
Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10566201 and Search Result us-10-566-201-2.rge.

Go Back to previous page

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OM nucleic - nucleic search, using sw model

Run on: September 28, 2006, 01:51:24 ; Search time 11528 Seconds
(without alignments)
6800.793 Million cell updates/sec

Title: US-10-566-201-2
Perfect score: 1226
Sequence: 1 gatctctatgtatataaaaa.....ttgactaagcttaaacgacg 1226

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*

13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1226	100.0	1226	2	CS007929	CS007929 Sequence
	2	1226	100.0	1226	2	CS025770	CS025770 Sequence
c	3	1226	100.0	83650	4	AB023041	AB023041 Arabidops
	4	941	76.8	92620	4	AB026636	AB026636 Arabidops
	5	837	68.3	1700	2	AR488147	AR488147 Sequence
c	6	797.8	65.1	83646	4	AB005248	AB005248 Arabidops
	7	797.6	65.1	94487	4	AC012394	AC012394 Arabidops
c	8	797.6	65.1	100806	4	AC015450	AC015450 Arabidops
c	9	739.2	60.3	104386	4	ATT32A17	AL161813 Arabidops
c	10	739.2	60.3	179771	4	ATCHRIV25	AL161513 Arabidops
	11	691	56.4	95519	4	AF071527	AF071527 Arabidops
c	12	691	56.4	116448	4	AC005142	AC005142 Arabidops
c	13	691	56.4	159629	4	ATCHRIV9	AL161497 Arabidops
c	14	553.2	45.1	95190	4	AC007203	AC007203 Arabidops
	15	231.8	18.9	105223	4	AC007399	AC007399 Arabidops
c	16	114.6	9.3	349980	2	AX344555	AX344555 Sequence
	17	112	9.1	175544	12	AC117342	AC117342 Rattus no
	18	111.2	9.1	4660	2	CS083843	CS083843 Sequence
	19	111.2	9.1	90550	5	AL592166	AL592166 Human DNA
c	20	108.8	8.9	109786	4	F5K24	AF128395 Arabidops
c	21	108.8	8.9	183181	4	ATCHRIV19	AL161507 Arabidops
	22	107.6	8.8	1524	2	CS083838	CS083838 Sequence
	23	107.6	8.8	212999	12	AC151201	AC151201 Bos tauru
c	24	107.4	8.8	170627	12	AC125567	AC125567 Rattus no
c	25	106.4	8.7	15548	2	AX347057	AX347057 Sequence
	26	105.8	8.6	47403	2	AX059535	AX059535 Sequence
	27	105.8	8.6	91470	4	T4B21	AF118223 Arabidops
	28	105.8	8.6	110000	2	AR777056_04	Continuation (5 of
	29	105.8	8.6	200001	4	ATCHRIV13	AL161501 Arabidops
	30	105.6	8.6	154563	5	CR936360	CR936360 Human DNA
c	31	104.4	8.5	2131	2	CS083950	CS083950 Sequence
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	33	104.2	8.5	241619	12	AC167751	AC167751 Bos tauru
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c	35	103.2	8.4	7218	2	I66494	I66494 Sequence 14
c	36	101.6	8.3	143331	5	AC091214	AC091214 Homo sapi
c	37	100.8	8.2	169510	12	CR855864	CR855864 Danio rer
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	39	100.8	8.2	250531	13	AE014845	AE014845 Plasmodiu
	40	100.6	8.2	155942	12	AC136691	AC136691 Homo sapi
	41	100.6	8.2	161765	5	AC113190	AC113190 Homo sapi
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c	43	100.2	8.2	192265	5	CNS018P3	AL110118 Human chr
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45 99.8 8.1 67970 13 PFMAL1P3 AL031746 Plasmodiu

ALIGNMENTS

RESULT 3
AB023041/c
LOCUS AB023041 83650 bp DNA linear PLN 14-FEB-2004
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11.
ACCESSION AB023041 BA000014
VERSION AB023041.1 GI:4220640
KEYWORDS .
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS **Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.**
TITLE Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones
JOURNAL **DNA Res. 7 (2), 131-135 (2000)**
PUBMED 10819329
REFERENCE 2 (bases 1 to 83650)
AUTHORS Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MPE11
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is K9I22 and the 3' clone is MJL14.
FEATURES Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1226;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      11869 TTTTTCTTGACTAAGCTTAAACGACG 11844
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APPENDIX B

SCORE Search Results Details for Application 10566201 and Search Result us-10-566-201-1.rge.
Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10566201 and Search Result us-10-566-201-1.rge.

Go Back to previous page

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: October 19, 2006, 02:01:17 ; Search time 6423 Seconds
(without alignments)
10284.553 Million cell updates/sec

Title: US-10-566-201-1
Perfect score: 1033
Sequence: 1 gaattcgtggtatagcgtta.....aaatcaatcactttctctaa 1033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*

14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1033	100.0	1033	2	CS007928	CS007928 Sequence
	2	1033	100.0	1033	2	CS025769	CS025769 Sequence
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	4	1033	100.0	121668	4	AC022521	AC022521 Arabidops
	5	144.4	14.0	98461	4	ATT6H20	AL096859 Arabidops
	6	142.6	13.8	100906	4	ATF24G16	AL138647 Arabidops
	7	142.4	13.8	89219	4	ATT6K22	AL031187 Arabidops
	8	142.4	13.8	198715	4	ATCHRIV54	AL161554 Arabidops
c	9	140.6	13.6	99254	4	AC002423	AC002423 Genomic s
	10	140.4	13.6	100867	4	AC008047	AC008047 Genomic s
	11	140.2	13.6	78181	4	AB011477	AB011477 Arabidops
	12	139.6	13.5	102299	4	AC018908	AC018908 Arabidops
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	17	133.8	13.0	199667	4	ATCHRIV37	AL161537 Arabidops
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c	25	130.4	12.6	99698	4	AC008262	AC008262 Genomic s
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	28	128.2	12.4	89811	4	AC018849	AC018849 Arabidops
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ALIGNMENTS

RESULT 3
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LOCUS AC064879 109180 bp DNA linear PLN 19-AUG-2000
DEFINITION Arabidopsis thaliana chromosome I BAC T6A9 genomic sequence, complete sequence.
ACCESSION AC064879
VERSION AC064879.3 GI:7958959
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
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REFERENCE 1 (bases 1 to 109180)
AUTHORS **Federspiel**,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S., Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M., Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 109180)
AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E., Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE 3 (bases 1 to 109180)
AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E., Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE 4 (bases 1 to 109180)
AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (19-AUG-2000) DNA Sequencing and Technology Center,

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            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     On May 20, 2000 this sequence version replaced gi:7922104.
            Bases 1-51,564 of clone T6A9 overlap with bases 55,373-106,937 of
            BAC clone T7I23 (gb|U89959) and bases 91,185-109,180 overlap with
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